SEQUENCE LISTING

COPY

(1) GENERAL INFORMATION:

    (i) APPLICANT: Reed, John C.
                Sato, Takaaki

    (ii) TITLE OF INVENTION: CD40 Associated Proteins

   (iii) NUMBER OF SEQUENCES: 17

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    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: US 08/349,357
        (B) FILING DATE: 02-DEC-1994
        (C) CLASSIFICATION:

   (viii) ATTORNEY/AGENT INFORMATION:
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        (C) REFERENCE/DOCKET NUMBER: P-LJ 1203

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(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2240 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 137..1766

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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AGAAGTGATG CCACTTGGTT AAGGTCCCAG AGCAGGTCAG AATCAGACCT AGGATCAGAA        60

ACCTGGCTCC TGGCTCCTGG CTCCCTACTC TTCTAAGGAT CGCTGTCCTG ACAGAAGAGA       120

ACTCCTCTTT CCTAAA ATG GAG TCG AGT AAA AAG ATG GAC TCT CCT GGC          169
                  Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly
                   1               5                  10

GCG CTG CAG ACT AAC CCG CCG CTA AAG CTG CAC ACT GAC CGC AGT GCT        217
Ala Leu Gln Thr Asn Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala
           15                  20                  25
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GGG ACG CCA GTT T    TC CCT GAA CAA GGA GGT TAC AA  AA AAG TTT        265
Gly Thr Pro Val P    al Pro Glu Gln Gly Gly Tyr Ly  lu Lys Phe
        30              35                   40

GTG AAG ACC GTG GAG GAC AAG TAC AAG TGT GAG AAG TGC CAC CTG GTG        313
Val Lys Thr Val Glu Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val
        45              50                  55

CTG TGC AGC CCG AAG CAG ACC GAG TGT GGG CAC CGC TCC TGC GAG AGC        361
Leu Cys Ser Pro Lys Gln Thr Glu Cys Gly His Arg Ser Cys Glu Ser
 60              65                  70                      75

TGC ATG GCG GCC CTG CTG AGC TCT TCA AGT CCA AAA TGT ACA GCG TGT        409
Cys Met Ala Ala Leu Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys
            80                  85                  90

CAA GAG AGC ATC GTT AAA GAT AAG GTG TTT AAG GAT AAT TGC TGC AAG        457
Gln Glu Ser Ile Val Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys
                95                  100                 105

AGA GAA ATT CTG GCT CTT CAG ATC TAT TGT CGG AAT GAA AGC AGA GGT        505
Arg Glu Ile Leu Ala Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly
            110                 115                 120

TGT GCA GAG CAG TTA ACG CTG GGA CAT CTG CTG GTG CAT TTA AAA AAT        553
Cys Ala Glu Gln Leu Thr Leu Gly His Leu Leu Val His Leu Lys Asn
        125             130                 135

GAT TGC CAT TTT GAA GAA CTT CCA TGT GTG CGT CCT GAC TGC AAA GAA        601
Asp Cys His Phe Glu Glu Leu Pro Cys Val Arg Pro Asp Cys Lys Glu
140             145                 150                     155

AAG GTC TTG AGG AAA GAC CTG CGA GAC CAC GTG GAG AAG GCG TGT AAA        649
Lys Val Leu Arg Lys Asp Leu Arg Asp His Val Glu Lys Ala Cys Lys
                160                 165                 170

TAC CGG GAA GCC ACA TGC AGC CAC TGC AAG AGT CAG GTT CCG ATG ATC        697
Tyr Arg Glu Ala Thr Cys Ser His Cys Lys Ser Gln Val Pro Met Ile
            175                 180                 185

GCG CTG CAG AAA CAC GAA GAC ACC GAC TGT CCC TGC GTG GTG GTG TCC        745
Ala Leu Gln Lys His Glu Asp Thr Asp Cys Pro Cys Val Val Val Ser
            190                 195                 200

TGC CCT CAC AAG TGC AGC GTC CAG ACT CTC CTG AGG AGC GAG GGG ACA        793
Cys Pro His Lys Cys Ser Val Gln Thr Leu Leu Arg Ser Glu Gly Thr
205                 210                 215

AAC CAG CAG ATC AAG GCC CAC GAG GCC AGC TCC GCC GTG CAG CAC GTC        841
Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val Gln His Val
220                 225                 230                 235

AAC CTG CTG AAG GAG TGG AGC AAC TCG CTC GAA AAG AAG GTT TCC TTG        889
Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys Val Ser Leu
                240                 245                 250

TTG CAG AAT GAA AGT GTA GAA AAA AAC AAG AGC ATA CAA AGT TTG CAC        937
Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile Gln Ser Leu His
                255                 260                 265

AAT CAG ATA TGT AGC TTT GAA ATT GAA ATT GAG AGA CAA AAG GAA ATG        985
Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg Gln Lys Glu Met
            270                 275                 280

CTT CGA AAT AAT GAA TCC AAA ATC CTT CAT TTA CAG CGA GTG ATA GAC        1033
Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln Arg Val Ile Asp
        285                 290                 295
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AGC CAA GCA GAG A●●CTG AAG GAG CTT GAC AAG GAG A●●GG TCC TTC        1081
Ser Gln Ala Glu I●Leu Lys Glu Leu Asp Lys Glu I●rg Ser Phe
300            305                    310              315

CGG CAG AAC TGG GAG GAA GCA GAC AGC ATG AAG AGC AGC GTG GAG TCC        1129
Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser Val Glu Ser
                320                  325              330

CTC CAG AAC CGC GTG ACC GAG CTG GAG AGC GTG GAC AAG AGC GCG GGG        1177
Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys Ser Ala Gly
                335                  340              345

CAA GTG GCT CGG AAC ACA GGC CTG CTG GAG TCC CAG CTG AGC CGG CAT        1225
Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu Ser Arg His
                350                  355              360

GAC CAG ATG CTG AGT GTG CAC GAC ATC CGC CTA GCC GAC ATG GAC CTG        1273
Asp Gln Met Leu Ser Val His Asp Ile Arg Leu Ala Asp Met Asp Leu
                365                  370              375

CGC TTC CAG GTC CTG GAG ACC GCC AGC TAC AAT GGA GTG CTC ATC TGG        1321
Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val Leu Ile Trp
380              385                  390              395

AAG ATT CGC GAC TAC AAG CGG CGG AAG CAG GAG GCC GTC ATG GGG AAG        1369
Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val Met Gly Lys
                400                  405              410

ACC CTG TCC CTT TAC AGC CAG CCT TTC TAC ACT GGT TAC TTT GGC TAT        1417
Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr Phe Gly Tyr
                415                  420              425

AAG ATG TGT GCC AGG GTC TAC CTG AAC GGG GAC GGG ATG GGG AAG GGG        1465
Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met Gly Lys Gly
            430                  435              440

ACG CAC TTG TCG CTG TTT TTT GTC ATC ATG CGT GGA GAA TAT GAT GCC        1513
Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu Tyr Asp Ala
            445                  450              455

CTG CTT CCT TGG CCG TTT AAG CAG AAA GTG ACA CTC ATG CTG ATG GAT        1561
Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met Leu Met Asp
460                  465              470              475

CAG GGG TCC TCT CGA CGT CAT TTG GGA GAT GCA TTC AAG CCC GAC CCC        1609
Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys Pro Asp Pro
                480                  485              490

AAC AGC AGC AGC TTC AAG AAG CCC ACT GGA GAG ATG AAT ATC GCC TCT        1657
Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn Ile Ala Ser
                495                  500              505

GGC TGC CCA GTC TTT GTG GCC CAA ACT GTT CTA GAA AAT GGG ACA TAT        1705
Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn Gly Thr Tyr
            510                  515              520

ATT AAA GAT GAT ACA ATT TTT ATT AAA GTC ATA GTG GAT ACT TCG GAT        1753
Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp Thr Ser Asp
525                  530                  535

CTG CCC GAT CCC T GATAAGTAGC TGGGGAGGTG GATTTAGCAG AAGGCAACTC        1806
Leu Pro Asp Pro
540

CTCTGGGGGA TTTGAACCGG TCTGTCTTCA CTGAGGTCCT CGCGCTCAGA AAAGGACCTT        1866

GTGAGACGGA GGAAGCGGCA GAAGGCGGAC GCGTGCCGGC GGGAGGAGCC ACGCGTGAGA        1926
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CACCTGACAC GTTTTA    T AGACTAGCCA CACTTCACTC TGAAGA    A TTTATCCTTC    1986

AACAAGCATA AATATTG  G TCAGAGAAGG TTTTCATTTT CATTTTTAAA GATCTAGTTA    2046

ATTAAGGTGG AAAACATATA TGCTAAACAA AAGAAACATG ATTTTTCTTC CTTAAACTTG    2106

AACACCAAAA AACACACACA CACACACACA CGTGGGGATA GCTGGACATG TCAGCATGTT    2166

AAGTAAAAGG AGAATTTATG AAATAGTAAT GCAATTCTGA TATCTTCTTT CTAAAATTCA    2226

AGAGTGCAAT TTTG                                                     2240
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(2) INFORMATION FOR SEQ ID NO:2:

.(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 543 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn
 1               5                  10                  15

Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe
            20                  25                  30

Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
        35                  40                  45

Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
    50                  55                  60

Gln Thr Glu Cys Gly His Arg Ser Cys Glu Ser Cys Met Ala Ala Leu
65                  70                  75                  80

Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
                85                  90                  95

Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala
            100                 105                 110

Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu
        115                 120                 125

Thr Leu Gly His Leu Leu Val His Leu Lys Asn Asp Cys His Phe Glu
    130                 135                 140

Glu Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys
145                 150                 155                 160

Asp Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr
            165                 170                 175

Cys Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His
            180                 185                 190

Glu Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys
        195                 200                 205

Ser Val Gln Thr Leu Leu Arg Ser Glu Gly Thr Asn Gln Gln Ile Lys
    210                 215                 220
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Ala His Glu Ala Ser     Ala Val Gln His Val Asn Leu Leu Lys Glu
225              230                 235                     240

Trp Ser Asn Ser Leu Glu Lys Lys Val Ser Leu Leu Gln Asn Glu Ser
                245                 250                 255

Val Glu Lys Asn Lys Ser Ile Gln Ser Leu His Asn Gln Ile Cys Ser
            260                 265                 270

Phe Glu Ile Glu Ile Glu Arg Gln Lys Glu Met Leu Arg Asn Asn Glu
        275                 280                 285

Ser Lys Ile Leu His Leu Gln Arg Val Ile Asp Ser Gln Ala Glu Lys
        290                 295                 300

Leu Lys Glu Leu Asp Lys Glu Ile Arg Ser Phe Arg Gln Asn Trp Glu
305                 310                 315                     320

Glu Ala Asp Ser Met Lys Ser Ser Val Glu Ser Leu Gln Asn Arg Val
            325                 330                     335

Thr Glu Leu Glu Ser Val Asp Lys Ser Ala Gly Gln Val Ala Arg Asn
            340                 345                 350

Thr Gly Leu Leu Glu Ser Gln Leu Ser Arg His Asp Gln Met Leu Ser
            355                 360                 365

Val His Asp Ile Arg Leu Ala Asp Met Asp Leu Arg Phe Gln Val Leu
    370                 375                 380

Glu Thr Ala Ser Tyr Asn Gly Val Leu Ile Trp Lys Ile Arg Asp Tyr
385                 390                 395                     400

Lys Arg Arg Lys Gln Glu Ala Val Met Gly Lys Thr Leu Ser Leu Tyr
            405                 410                     415

Ser Gln Pro Phe Tyr Thr Gly Tyr Phe Gly Tyr Lys Met Cys Ala Arg
            420                 425                 430

Val Tyr Leu Asn Gly Asp Gly Met Gly Lys Gly Thr His Leu Ser Leu
        435                 440                 445

Phe Phe Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu Pro Trp Pro
    450                 455                 460

Phe Lys Gln Lys Val Thr Leu Met Leu Met Asp Gln Gly Ser Ser Arg
465                 470                 475                     480

Arg His Leu Gly Asp Ala Phe Lys Pro Asp Pro Asn Ser Ser Ser Phe
            485                 490                 495

Lys Lys Pro Thr Gly Glu Met Asn Ile Ala Ser Gly Cys Pro Val Phe
            500                 505                 510

Val Ala Gln Thr Val Leu Glu Asn Gly Thr Tyr Ile Lys Asp Asp Thr
            515                 520                 525

Ile Phe Ile Lys Val Ile Val Asp Thr Ser Asp Leu Pro Asp Pro
    530                 535                 540
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAATTCAAA AAGGTGGCCA AG   22

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGATCATCAC TGTCTCTCCT GCAC   24

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGAATTCAAG GCCCCCCACC CCAAG   25

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGATCAACTC TCTTTGCCAT CCTC   24

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGAATTCAAG AGAAAGGAAG TACAG   25

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGATCACTA GACCAAGCTT TGGAT   25

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAATTCAAA AAGAAGCCCT TGTGCCT   27

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTCGACTTA ACTGGGCTTC ATCCCA   26

64

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGATCCGCT ACCAACGGTG GAAG   24

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTCGACTCA TCTGAGAAGA CTGGG   25

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 54 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TAATACGACT CACTATAGGG AGACCACATG GATGATGTAT ATAACTATCA TTTC 54

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTACCAGAAT TCGGCATGCC GGTAGAGGTG TGGTCA   36

(2) INFORMATION FOR SEQ ID NO:15:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGTTAACTG CTCTGCACAA   20

(2) INFORMATION FOR SEQ ID NO:16:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTACATTTTG GACTTGAAGA   20

(2) INFORMATION FOR SEQ ID NO:17:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 28 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCCCGG GGATCCGTCG ACCTGCAG   28